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Elevated rates of opsin amino acid evolution following gene duplication in Lycaena butterflies (Lepidoptera)

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regulation mechanisms of host immune disruption and developmental arrest induced by *T. nigriceps* parasitism. The functional analysis of some of these genes indicates that they are involved in immune suppression, by inducing apoptosis of haemocytes or by disrupting NF-κB signalling pathways. This latter alteration is determined by IκB-like (ANK) proteins, similar to those of insects and mammals, but characterized by shorter ankyrin domains and by the absence of regulatory domains. The phylogenetic analysis of PDV ANK proteins indicates that they have a common origin, even though BVs and IVs are thought to be unrelated. The evolutionary implications of this finding are discussed.

Elevated rates of opsin amino acid evolution following gene duplication in *Lycaena* butterflies (Lepidoptera)

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The process by which genes acquire new functions is not well understood, but gene duplication is considered an important mechanism for generating functional diversity. Gene duplications are often followed by an accelerated rate of evolution. We tested this hypothesis by examining the evolution of a pair of blue opsin duplicate genes in the butterfly genus *Lycaena*. Visual pigments are the light-sensitive molecules in the arthropods' compound eye. The specific amino acid sequence of the opsin protein determines the peak absorption maximum of the visual pigment. We used PCR, cloning and sequencing of eye derived cDNAs to characterize all four opsin genes of *L. heteronea* and *L. helloides*, which we combined with the previously characterized *L. rubidus* opsin sequences. The translated opsin amino acid sequences were aligned and used to construct a phylogenetic tree. Each of these sequences falls within one of three well-supported clades in the insect opsin gene tree, comprised respectively of ultraviolet (UV), blue (B) and long-wavelength (LW) sensitive pigments. One of these genes belongs to the ultraviolet (UV) opsin clade, and encodes the visual pigment with peak sensitivity to 360 nm. A second gene clusters within the long wavelength (LW) clade and corresponds to the visual pigment with peak sensitivity to 568 nm. Two genes clustered within the blue-sensitive opsin clade (B1 and B2), representing respectively the visual pigments with peak sensitivity to 437 (blue) and 500 (green) nm. We used Tajima's (1993) method to test whether or not the P500 opsin displayed an elevated rate of amino acid evolution following its divergence from the P437 opsin, which has a more typical peak sensitivity for opsins of that clade. Visual inspection of the branch lengths of the opsin tree suggested that B1 and B2 are evolving at different rates, and results from Tajima's test support this finding for all three *Lycaena* species ($p<0.05$ for all species). A second analysis separating the transmembrane (TM) and the non-transmembrane (Non-TM) domains of the opsin protein, shows that only the amino acid differences between the TM domains are responsible for this different rate of evolution between B1 and B2 in all three species (TM domains $p<0.01$, Non-TM domains $p>0.4$), further suggesting that one of these genes has evolved a new function.

Embryonic development and wing colour patterns in the tropical butterfly, *Bicyclus anynana*

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Butterfly wing patterns provide an attractive system for studying interactions between the evolutionary and developmental processes that shape morphological variation. The African butterfly *Bicyclus anynana* with its conspicuous eyespots has been established as an "evo-devo" laboratory model and successfully used to study the genetic mechanisms underlying variation in wing patterns. The problem, however, is that none of the insect model species has eyespot patterns which appear to be a Lepidoptera-specific trait. Genetic comparison and identification of the genes involved in colour pattern formation become a challenge when genomic resources are only starting to be developed. Over twenty mutant stocks with dramatically altered eyespot pattern are maintained in our laboratory and several of them appear to have disturbed embryonic development. Examination of the genes with such

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